What is claimed is:

1. A substantially pure polypeptide characterized as:
   (a) phosphorylating Cdc25 or a homologue thereof;
   (b) having a molecular mass of about 58 kD;
   (c) having about 517 amino acids;
   (d) having SQ/TQ motifs at the amino terminal region;
   (e) having a carboxyl terminal kinase domain; and
   (f) having an amino terminal forkhead-associated domain.

2. A polypeptide of claim 1, wherein the polypeptide has an amino acid sequence as set forth in SEQ ID NO:2.

3. A substantially pure polypeptide having an amino acid sequence as set forth in SEQ ID NO:2 or conservative variants thereof.

4. A substantially pure polypeptide having an amino acid sequence that is about 80% homologous to the polypeptide of claim 3.

5. An isolated polynucleotide encoding a polypeptide of claim 1.

6. An isolated polynucleotide selected from the group consisting of:
   (a) a polynucleotide encoding a polypeptide having an amino acid sequence as set forth in SEQ ID NO:2;
   (b) a polynucleotide of (a), wherein all T's are U;
   (c) a polynucleotide complementary to (a) or (b);
   (d) a polynucleotide having a nucleotide sequence as set forth in SEQ ID NO:1; and
   (e) degenerate variants of (a), (b), (c) or (d).

7. An isolated polynucleotide having at least 15 continuous base pairs that hybridizes to a polynucleotide selected from the group consisting of:

(a) a polynucleotide encoding a polypeptide having an amino acid sequence as set forth in amino acids 1 to 86 or amino acids 461 to 517 of SEQ ID NO:2;

(b) a polynucleotide of (a), wherein T can be U;

(c) a polynucleotide complementary to (a) or (b);

(d) a polynucleotide having a nucleotide sequence as set forth in nucleotides 224 to 481 or nucleotides 1604 to 1770 of SEQ ID NO:1; and

(e) degenerate variants of (a), (b), (c) or (d).

8. An isolated polynucleotide at least 15 bases in length which hybridizes under moderately to highly stringent conditions to DNA encoding a polypeptide as set forth in SEQ ID NO:2.

9. An isolated polynucleotide according to claim 8, wherein the polynucleotide is antisense nucleic acid.

10. An isolated oligonucleotide as set forth in SEQ ID NO:3.

11. An isolated oligonucleotide as set forth in SEQ ID NO:4.

12. An isolated oligonucleotide as set forth in SEQ ID NO:5.

13. An antibody that binds to a polypeptide of claim 1 or binds to immunoreactive fragments thereof.

14. The antibody of claim 13, wherein the antibody is polyclonal.

15. The antibody of claim 13, wherein the antibody is monoclonal.

16. An expression vector comprising a polynucleotide of claim 5.

17. The expression vector of claim 16, wherein the vector is virus-derived.

18. The expression vector of claim 16, wherein the vector is plasmid-derived.

19. A host cell comprising a vector of claim 16.

20. A method for producing a polypeptide comprising the steps of:
    (a) culturing a host cell of claim 19 under conditions suitable for the expression of the polypeptide; and
    (b) recovering the polypeptide from the host cell culture.

21. A transgenic non-human animal having a transgene that expresses a polypeptide of claim 1 chromosomally integrated into the germ cells of the animal.

22. The transgenic animal of claim 25, wherein the animal is murine.

23. A method for increasing mitotic delay in a vertebrate cell comprising providing to the cell one or more oligonucleotides that form double-stranded DNA.

24. The method of claim 23, wherein the one or more oligonucleotides have the sequence set forth in SEQ ID NO:3 and SEQ ID NO:.

25. The method of claim 23, wherein the one or more oligonucleotide has the sequence set forth in SEQ ID NO:5.

26. A method for identifying a reagent that modulates phosphorylation of a polypeptide comprising:
    (a) incubating a reagent with the polypeptide, and one or more oligonucleotides that form double-stranded DNA, under conditions that allow the components to interact with each other; and
    (b) comparing the phosphorylation of the polypeptide to phosphorylation of a polypeptide not incubated with the reagent, wherein a difference in phosphorylation is indicative of a reagent that modulates phosphorylation of the polypeptide.

27. The method of claim 26, wherein the modulation is an increase in phosphorylation.

28. The method of claim 26, wherein the modulation is a decrease in phosphorylation.

29. The method of claim 26, wherein the polypeptide is Xenopus Cds1.

30. The method of claim 26, wherein the polypeptide is human Cds1.

31. The method of claim 26, wherein the one or more oligonucleotides have a sequence as set forth in SEQ ID NO:3 and SEQ ID NO:4.

32. The method of claim 26, wherein the one oligonucleotide has a sequence as set forth in SEQ ID NO:5.

33. The method of claim 26, wherein the reagent is selected a peptide, a peptidomimetic, a polypeptide, a pharmaceutical, a chemical compound, a polynucleotide or an antibody.

34. A method for modulating cell cycle progression in a cell, said method comprising providing to the cell a compound that affects the activity or expression of a Cds1 polypeptide, thereby modulating cell cycle progression.

35. The method of claim 34, wherein modulation of cell cycle progression is inhibition or a reduction in progression.

36. The method of claim 34, wherein the compound is a peptide, a peptidomimetic, a polypeptide, a pharmaceutical, a chemical compound, a polynucleotide, or an antibody.

37. The method of claim 34, wherein the polynucleotide is double-stranded DNA.

38. A method of treating a subject having a cellular disorder associated with increased cell cycle progression compared to a subject not having the cellular disorder, comprising administering to a subject having the disorder a therapeutically effective amount of a reagent that increases a Cds1 polypeptide activity, thereby treating the cellular disorder.

39. The method of claim 38, wherein the disorder is a cell proliferative disorder.

40. The method of claim 38, wherein the reagent is double-stranded DNA.

41. The method of claim 38, wherein the reagent is poly$(dT)_{40}$.

42. A method of diagnosing a Cds1- associated disorder in a subject comprising determining the level of Cds1 mRNA or protein expression in the subject, wherein a low level of Cds1 in the subject compared to the level in a subject not having a Cds-associated disorder is indicative of a Cds-associated disorder.

43. A kit for activating a Cds1 polypeptide comprising

(a) double-stranded DNA; and

(b) a container for the DNA.

44. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence selected from the group consisting SEQ ID NO:2, and sequences substantially identical thereto.

45. The computer system of claim 44, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

46. The computer system of claim 44, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

47. A method for comparing a first sequence to a reference sequence wherein said first sequence is a nucleic acid sequence selected from the group consisting SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence selected from the group consisting of SEQ ID NO:2, and sequences substantially identical thereto comprising:

(a) reading the first sequence and the reference sequence through use of a computer program which compares sequences; and

(b) determining differences between the first sequence and the reference sequence with the computer program.

48. The method of claim 47, wherein determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.